

Category	: International Rice Research Conference
Select Theme	: Genetic improvement
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Keyword 1	: Genomic selection
Keyword 2	: Marker-assisted selection
Keyword 3	: Genomics-assisted breeding
Title of Entry	: Genome-wide association studies for grain size and shape in Indica Rice MAGIC population
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Abstract	: Grain size and shape are very important quality traits which determines millers and consumers acceptance, hence first criteria for rice quality that breeders consider in developing new varieties for release and commercial production. The present study on Genome-wide association mapping was conducted to identify the quantitative trait loci (QTLs) for grain shape traits viz., kernel length (KL), kernel breadth (KB), kernel length to breadth ratio (KLBR) by using 395 advanced introgressed lines (AILs) generated through Multiparent Advanced Generation Inter Cross (MAGIC) approach by using 8 indica parents (founder lines) at International Rice Research Institute (IRRI), Philippines. The material was evaluated during Rabi 2016-17 in augmented RBD at RARS, Maruteru, Andhra Pradesh, India. Genotyping by sequencing (GBS) was done using ApeKI and a set of 96 samples per lane was sequenced on an Illumina HiSeq at Cornell University. SNP calls were made using Nipponbare as reference. The GBS technology provided 27,041 polymorphic SNP marker sites across all 12 chromosomes. Genome wide association study (GWAS) was carried out by using phenotypic and genotypic data through mixed linear model (MLM) and general linear model (GLM) in Trait analysis by aSSociation, Evolution and Linkage (TASSEL). In GWAS, a total of ten known QTLs were identified for the traits under study. Four QTLs viz., qGL-3a, GL3.1, qGL3, gl3a were identified on chromosome 3 which have reported earlier for kernel length. For KB, one QTL (qWIJ-2) on chromosome 2 and one QTL (grb7-2) were identified from the present study. Whereas for KLBR, 3 QTLs viz., qLWR-3 and gw3a (on chromosome 3) and one QTL gw7 (on chromosome 7) were identified. In addition to the above previously identified QTLs, four QTLs viz., qKL11 on chromosome 11 for KL, qKB2 on chromosome 2 for KB, qLBR5 on chromosome 5 and qLBR7 on chromosome 7 for LBR were identified as novel QTLs in this study. Fine mapping of QTLs can be done to achieve more precision and it may allow detection of QTLs with smaller effects which may prove useful for the development of reliable markers for marker assisted selection.

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